IMPROVEMENT IN SCREENING FOR RESISTANCE TO *SCLEROTINIA SCLEROTIORUM* IN COMMON BEAN THROUGH CHARACTERIZATION OF THE PATHOGEN AND UTILIZATION OF MULTI-STATE NUSERIES

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Sclerotinia sclerotiorum, cause of white mold in common bean, has over 400 host species, and resistance is rare among its many hosts. There is no complete resistance to *S. sclerotiorum* in common bean. A lack of adapted resistance sources inhibits progress in breeding cultivars with white mold resistance. Repeatability of resistance expression has been a consistent problem in screening putative sources of white mold resistance. Screening difficulties can be reduced by using multiple location screening sites and understanding the role of pathogen variation in the screening system.

In major bean production areas in the United States, the bean breeder or plant pathologist at each different location uses their own standard screening isolate for greenhouse/laboratory tests. Often, these isolates have not been selected, but rather they are collected from cull piles (bean debris including sclerotia discarded from harvested fields). The genetic variation or variation in aggressiveness in these isolates from site to site has never been addressed. Nine isolates used in greenhouse screening and control isolate 1980 (the isolate of *S. sclerotiorum* that has been sequenced) were subjected to the mycelial compatibility groupings (MCGs) and aggressiveness tests. Also, isolates of *S. sclerotiorum* were collected from white mold field screening nurseries across nine states/countries; isolates were collected from G122 (more resistant), Bunsi (intermediate), and Beryl (susceptible) in each of three reps at the nine different screening sites from 2003-2005.

MCGs were used to test the isolates for clonality. If the different isolates grew together and formed a continuous mycelial mat on DS medium, the isolates were compatible and considered clonal. If the isolates formed a barrage line of dead cells where the hyphae met, the isolates were incompatible, and each isolate was considered unique. The ten greenhouse screening isolates formed six MCGs. MCG A was composed of clonal screening isolates from Nebraska, Oregon, and the control isolate. MCG B was formed by the Wisconsin and New York greenhouse screening isolates. MCG C contained the Colorado and North Dakota screening isolates. MCG D, MCG E, and MCG F were formed by the single screening isolates from Michigan, Idaho, and Washington, respectively. When the ten greenhouse isolates and the 146 field screening isolates were tested by the MCG assay, high variation was found within and between field locations. Sixty-four MCGs were identified when the 156 total isolates were tested; 36 of those MCGs (over half) were composed of a single isolate; and 6 of the 64 MCGs were formed by screening isolates from more than one location, i.e. an MCG was formed by greenhouse screening isolates, Minnesota field isolates, and Washington field isolates. MCG A and MCG B, two greenhouse screening MCGs, were clonal with isolates from field screening sites from different nursery locations. Greenhouse screening isolates MCG C, MCG D, and MCG F were clonal with at least one field screening isolate from the same location, i.e. the Michigan greenhouse screening isolate was clonal with at least one Michigan field screening isolate.

MCG E, formed by the Idaho screening isolate, was completely unique, and was not compatible with any of the other 155 isolates.

Genetic variation found by testing isolates using the MCGs varied by location. California and Washington had high within field variation. On the other hand, all eleven Minnesota isolates fit into two clonal groups, thus there was lower genetic variability at this location.

Unless genetic variation reflects the ability of the pathogen to cause disease (affects aggressiveness or virulence), this information is not likely to impact bean breeders and pathologists that screen for white mold resistance. Aggressiveness was tested in the isolates of *S. sclerotiorum* by the straw test (Petzoldt and Dickson, 1996). The stem of the bean plant was cut approx. 1" above the 4th node, and a straw filled with inoculum was placed over the cut end of the plant. The spread of the pathogen down the stem is measured after 8 days using a rating scale (Teran et al, 2005), 1=least aggressive and 9=most aggressive.

First, the ten greenhouse isolates were tested on cultivar G122. Then, the ten greenhouse isolates were tested on ten cultivars of different seed classes (different white mold resistance backgrounds). Finally, the 156 total screening isolates were also tested on cultivar G122. In all tests, significant differences were found between the isolates. However, when the isolate aggressiveness was compared to the MCGs the isolates came from, the MCGs were significantly different, but the isolates within MCGs did not differ in aggressiveness. This data supports the hypothesis that the differences in aggressiveness can be attributed to the MCG that the screening isolates form. The most aggressive MCG caused a straw test rating of 7.50 (susceptible reaction), and the least aggressive MCG caused a straw test rating of 2.92 (resistant reaction). Thus, the differences in aggressiveness caused by genetic variation in the isolates were important to consider when screening for resistance.

Pathogen variability exists in both greenhouse and field screening isolates. Use of the multi-site can provide more convincing evidence for putative resistance in bean lines. We recommend that a common greenhouse isolate(s) be selected for screening across locations.

REFERENCES

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